

Figure 1

Map of Human CD20/IgE-Receptor Like cDNA (SEQ ID NO: 1) and
Amino Acid Sequence (SEQ ID NO: 2)
(Agp-96614-a1)
(CD20RP2)

5

1	TTCCAGTGCTCCAGGCAGCCTCAGCACAAAGAAAAGAACATGGTCTAGACTGAAGTACCAA	60
61	CTAAATCATCTCCTTTCAAATTATCACCGACACCATCATGGATTCAAGCACCGCACACAG	120
1	M D S S T A H S	8
121	TCCGGTGTCTTCTGGTATTTCTCCAGAAATCACTGCTTCAGAATATGAGTCCACAGAACT	180
9	P V F L V F P P E I T A S E Y E S T E L	28
181	TTCAGCCACGACCTTTTCAACTCAAAGCCCCTTGCAAAAATTATTTGCTAGAAAAATGAA	240
29	S A T T F S T Q S P L Q K L F A R K M K	48
241	AATCTTAGGGACTATCCAGATCCTGTTTGGAAATTATGACCTTTTCTTTTGGAGTTATCTT	300
49	I L G T I Q I L F G I M T F S F G V I F	68
301	CCTTTTCACTTTGTAAAAACCATATCCAAGGTTTCCCTTTATATTTCTTTTCAAGATATCC	360
69	L F T L L K P Y P R F P F I F L S G Y P	88
361	ATTCTGGGGCTCTGTTTGTTCATTAATTCTGGAGCCTTCCTAATTGCAGTGAAAAGAAA	420
89	F W G S V L F I N S G A F L I A V K R K	108
421	AACCACAGAAACTCTGATAATATTGAGCCGAATAATGAATTTTCTTAGTGCCCTGGGAGC	480
109	T T E T L I I L S R I M N F L S A L G A	128
481	AATAGCTGGAATCATTCTCCTCACATTTGGTTTCATCCTAGATCAAAACTACATTTGTGG	540
129	I A G I I L L T F G F I L D Q N Y I C G	148
541	TTATTCTCACCAAAATAGTCAGTGTAAGGCTGTTACTGTCCTGTTCTTGGGAATTTTGAT	600
149	Y S H Q N S Q C K A V T V L F L G I L I	168
601	TACATTGATGACTTTTCAGCATTATTGAATTATTCATTTCTCTGCCTTTCTCAATTTGGG	660
169	T L M T F S I I E L F I S L P F S I L G	188
661	GTGCCACTCAGAGGATTGTGATTGTGAACAATGTTGTTGACTAGCACTGTGAGAATAAAG	720
189	C H S E D C D C E Q C C *	201
721	ATGTGTTAAATCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	760

Figure 2

Map of Human CD20/IgE-receptor Like cDNA (SEQ ID NO: 3) and
Amino Acid Sequence (SEQ ID NO: 4)

(Agp-69406-a1)

(CD20RP1)

1	GGCAGGAACAGCCAGTGGGAGGTTCCAGCTGAGCGCTCCCCAGAGGTGAGCTGATCCCCA	60
61	GCCACAGCACACAGGACCAGGCTGCGAGAACAGCATCATCAGCATCATGCTATTACAATC	120
1		M L L Q S 5
121	CCAAACCATGGGGGTTTCTCACAGCTTTACACCAAAGGGCATCACTATCCCTCAAAGAGA	180
6	Q T M G V S H S F T P K G I T I P Q R E	25
181	GAAACCTGGACACATGTACCAAAACGAAGATTACCTGCAGAACGGGCTGCCAACAGAAAC	240
26	K P G H M Y Q N E D Y L Q N G L P T E T	45
241	CACCGTTCTTGGGACTGTCCAGATCCTGTGTTGCCTGTTGATTTCAAGTCTGGGGGCCAT	300
46	T V L G T V Q I L C C L L I S S L G A I	65
301	CTTGGTTTTTGTCTCCCTACCCCTCCCACTTCAATCCAGCAATTTCCACCACTTTGATGTC	360
66	L V F A P Y P S H F N P A I S T T L M S	85
361	TGGGTACCCATTTTATAGGAGCTCTGTGTTTGGCATTACTGGATCCCTCTCAATTATCTC	420
86	G Y P F L G A L C F G I T G S L S I I S	105
421	TGGAAAACAATCAACTAAGCCCTTTGACCTGAGCAGCTTGACCTCAAATGCAGTGAGTTC	480
106	G K Q S T K P F D L S S L T S N A V S S	125
481	TGTTACTGCAGGAGCAGGCCTCTTCTCCTTGCTGACAGCATGGTAGCCCTGAGGACTGC	540
126	V T A G A G L F L L A D S M V A L R T A	145
541	CTCTCAACATTGTGGCTCAGAAATGGATTATCTATCCTCATTGCCTTATTCGGAGTACTA	600
146	S Q H C G S E M D Y L S S L P Y S E Y Y	165
601	TTATCCAATATATGAAATCAAAGATTGTCTCCTGACCAGTGTGAGTTTAACAGGTGTCCT	660
166	Y P I Y E I K D C L L T S V S L T G V L	185
661	AGTGGTGATGCTCATCTTCACTGTGCTGGAGCTCTTATTAGCTGCATACAGTTCTGTCTT	720
186	V V M L I F T V L E L L L A A Y S S V F	205
721	TTGGTGGAACAGCTCTACTCCAACAACCTGGGAGTTCATTTTCTCGACCCAGTCACA	780
206	W W K Q L Y S N N P G S S F S S T Q S Q	225
781	AGATCATATCCAACAGGTCAAAAAGAGTTCTTCACGGTCTTGATATAAGTAACTCTTGG	840
226	D H I Q Q V K K S S S R S W I *	241
841	CCTCAGAGGAAGGAAAAGCAACTCAACACTCATGGTCAAGTGTGATTAGACTTTCCTGAA	900
901	ATCTCTGCCATTTTATAGATACTGTGAAACAACTAAAAAAAAAAGCTTTTGTGTTTGTATTT	960
961	GAAAAAAAAAAAAAAAAAAAAA	982

Figure 3

HTM	M---ASH-E	VDN---ABLG	SASA-----	HGTGSETGP	EEL-MT---S	32
HTGERB	HGTYSRHR	PEE---STFS	AAMTTNGME	QANPGAGPV	POLGMM---A	44
HURP4	M---TSQPV	PNE---TUV	LPS-----	NWIFSOABK	PE-----P	29
69406	M---LLQSQ	TMG---VSHS	FTP-----	KGTI POREK	PG-----H	29
I qERbet a	MD---TESNR	RAH---LALP	QEPSSVPAT-	EVLEI SRQEV	SSGRLL---K	40
66614	M---DSSTA	HSP---VFLV	FPF-----	-EI TASEYES	TEL-SA---T	31
HTPEF86	MHSMVAVPV	ANSVLVAFH	NGV PVTGIM	SHVPL VPHSO	POVHLVRGMP	50
6020	MTTFMSV--	-----N	GTF PAEP- MK	GPI ANKSGRK	P---LFR RM	34
HTMZF5	MDTGGA---	-----	ROVGL-----	-----	-----	12
HTAL6	MDYGGA---	-----	ROI GH-----	-----	-----	12
Canz enz w	M-----	-----	-----	-----	-----	50
HTM	VYHPI--NBS	PD-YOKAMLR	VLGAVQLNA	AMLALGBFL	GSLQIPIMFQ	79
HTGERB	VI HSLKXGL	QKTLKSEPK	VLGVVQLTA	LMLSMGTIM	PCMA-SNEYG	93
HURP4	TNOGQ--DSL	KK-HLHAKK	VI GTI Q LQG	MYLSLG IL	ASASFSRIFT	76
69406	MYONE--DYL	QH-GLPTETT	VLGTWQLCO	LLI SSLGAIL	VFAFPYSHFN	76
I qERbet a	SASSPLHFW	LT-VLKKEZE	FLGVYQLTA	M QLOFGEW	OSVLDI SHIE	89
66614	TFSTQ--SPL	QK-LFARIMK	ILGTIQLFG	IMTFSFQIF	LFTL-LMPYP	77
HTPEF86	PSLVSNNGQ	PVKALKKSK	TLGAVQLIG	LAH GLGSIM	ATVL-VGEYL	99
6020	SSLVG--PTQ	TF--FMRESK	TLGAVQLHNS	LHM ALGSUL	-M P-AGVA	78
HTMZF5	-SLI T-----	-----L---	QVCI -VANA	LLVPHNE--	-TSW-TM--N	41
HTAL6	-SLVG-----	-----L---	ALLCI -AARN	LLVPHNE--	-TKY-ASE-N	41
Canz enz w	-----	-----E.	.LG.IGL.	L....G..	-----	100
HTM	KHFFFTFYT	GYPIWGAIFT	OSSGTLSVIA	Q KP-----	-----T-	114
HTGERB	SN--PI SVI	GYTIWGAIFT	II SSGSL AA	Q PT-----	-----T-	126
HURP4	QV-TSTLLNS	AWPI GEPFF	II SSGSL AT	EXPL-----	-----T-	110
69406	PA-I STTLNE	GYFFL GALCF	Q T SSGSL IS	QKPS-----	-----T-	110
I qERbet a	QD-I FSSFKA	GYFFWGAIFT	SI SSGSL IS	ERPN-----	-----A-	123
66614	R--FFPI FLS	GYFFWGAIFT	INSGLRI AV	KPKT-----	-----T-	110
HTPEF86	SI SFYGGF--	PF-W GGLNF	II SSGSLVAA	ENKP-----	-----Y-S	131
6020	PI QVTWVW--	PL-W GGLNF	II SSGSLAAT	ENKS-----	-----P-	109
HTMZF5	HL SLQWGLW	GF-I GGGILW	LQPGI AAWRA	QKQKQCGAG	QGN-----RC	85
HTAL6	HL SFFVWFFS	G-VGGSLIM	LLPAFVFI GL	EXDCCO--GD	QGHENCKKRC	88
Canz enz w	-----	GY...G...F	.ISG LSI .	-----	-----	150
HTM	-----	-----RW	I QNSTQNHIA	SATI ALVGBA	FLSLN AVN	147
HTGERB	-----	-----KL	VRSGLQHIT	SVILAAGSL	INTFLATY-	158
HURP4	-----	-----ML	VHSSLVSSLL	SALVALGB	ILSVKALIN	143
69406	-----	-----KFF	QLSSLTSHAV	SVITAGAGU	LLADSMALR	143
I qERbet a	-----	-----TVL	VRSGLQHITA	SSI AGGTGIT	ILI INLWKL	156
66614	-----	-----ETL	ILSRIMNPL	SALGAI AGU	LLTFGLDQ	143
HTPEF86	-----	-----YOL	LSGSLQHIFV	SM CSAWGV	LFI TDL---S	161
6020	-----	-----HCL	VKGRIMHSL	SLFAAI SGN	LSI MDI UNIK	142
HTMZF5	RMRSVFSSA	FQVLGAI YOL	SVSGRLRNG	FRCLMNGW	GVHFE---D	130
HTAL6	AMLSVL AAL	IG AGSGVOW	IYAAL Q.AEG	BLDLSLGGW	NITFA---S	134
Canz enz w	-----	-----L	...SLG NIA	S...A...G...	-----	200
HTM	OSLRCHSSS	E-----SPLOC	NWMS---I	SH-----	-GHVSL-LI	179
HTGERB	-SPH-H---	-----P-YC	NYVGM---S	NHOGTHSIL	HELQMA LL	199
HURP4	PASLOGLDK	N-N PTRSVV	SVF YHDLVT	TDQYAKAGL	AGTSLMLI	191
69406	TASQHGSEM	D-VLSSL PVS	ETVYP-IYEI	KDOLLTSVSL	TGVLVVMI	190
I qERbet a	AVIH-----	-----IHQD	KFF-----E	TKQFMASF	TEI VMMMLF	187
66614	NYI-----	-----C	GYSHQ---N	SXQKA-----	VTVLFLGIL	167
HTPEF86	IPH-----	-----PV	DVY-----	-----P--Y	ANGVNPMA	183
6020	I SHFLQESL	NFI PAHT PYI	N YHCPANP	SEKNSPSTQV	CYSI OSULG	192
HTMZF5	TAG-----	AVLLNRT LWD	ROE-----	-----AP--	PRVVPVNT	157
HTAL6	TEG-----	QVLLDTSTWS	ECT-----	-----EP--	KH VEWNVS	161
Canz enz w	-----	-----	.Y.-----	-----	-----L	250
HTM	LT LLELCVIT	STI AM-----	-----VON	-----ANCOH-S	-----	203
HTGERB	LSVLEFCI AV	SLSAF-----	-----GCK	-----VLCT-P	GGVILI UPSH	224
HURP4	QTLLEFLAV	LTAWL-----	-----PMK	-----DAYSDFP	GSVLF LRHSV	226
69406	FTVLELLAA	YSSVF-----	-----WMK	-----GLYSHNP	GSSFSSTQS-	224
I qERbet a	LTILGLGSV	SLTI C-----	-----GAG	-----EELKMGH	VPEDRVVEEL	222
66614	ITLMTFSIE	LFI SL-----	-----PFS	-----ILGCH	-----	190
HTPEF86	ISGVLLVFCL	LEFG-----	-----ACAS	SHFGGLVCO	-----QSSM	217
6020	ILSVML FAF	FOELVIAGV	ENE VKRQCSR	PKSN VLLSA	EKKKQTI EI	242
HTMZF5	LF SLVVAAC	LEI VL-----	-----C-	-----GLV	-----MTI	182
HTAL6	LF SL LALGG	IEPTL-----	-----C-	-----LI QV	-----NGVL	186
Canz enz w	...L L...-	-----	-----C-	-----	-----	300
HTM	--REI SSP-	P-N-----	--SV-----	-----	-----	214
HTGERB	SHMETSPT	PLN-----	--EV-----	-----	-----	239
HURP4	IGHNSQESKM	THD-----	--CGV BELLT	S-----	-----	248
69406	-QDM QGVKK	SSS-----	--RSM-----	-----	-----	240
I qERbet a	N YSATYSEL	EDP-----	--GEMPPID	L-----	-----	244
66614	--SEDDGCE-	--C-----	--CO-----	-----	-----	200
HTPEF86	--SVI VPM Y	AAMP-----	--VI T-----	--PDP	VTSPPSVSSE	245
6020	KEEVVLTET	SSOPKNEED	EII PI QEEEE	EETETNFPDP	PODQESPIE	292
HTMZF5	--GVFO---	-----	-----	-----	---GDCKKR	193
HTAL6	--GG C---	-----	-----	-----	---GDCSHR	197
Canz enz w	-----	-----	-----	-----	-----	350
HTM	-----	-----	-----	-----	-----	214
HTGERB	-----	-----	-----	-----	-----	239
HURP4	-----	-----	-----	-----	-----	248
69406	-----	-----	-----	-----	-----	240
I qERbet a	-----	-----	-----	-----	-----	244
66614	-----	-----	-----	-----	-----	200
HTPEF86	I QANK	-----	-----	-----	-----	250
6020	NDSSP	-----	-----	-----	-----	297
HTMZF5	DT-PH	-----	-----	-----	-----	197
HTAL6	QGYDC	-----	-----	-----	-----	202
Canz enz w	-----	-----	-----	-----	-----	355